

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>D. Schreiber</u>	NA Sequence (#) <u>13</u>	STN _____
Searcher Phone #: <u>272-2526</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>Rensselaer A61</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr Link _____
Date Completed: <u>9/27</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>15</u>	Fulltext _____	Sequence Systems <u>CompuLink</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>58</u>	Other _____	Other (specify) _____

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Schreiber, David

133C43

From: Schultz, James
Sent: Thursday, September 16, 2004 4:36 PM
To: Schreiber, David
Subject: score over length search request, 09/731,457

Hi David,

I need a score over length nucleotide sequence search on SEQ ID NO:73 in the above entitled case, which is a 20mer. I need the lower and upper limits to be 20 and 50, respectively, I need any hits that are above 65% complementarity, and please transfer as many hits into the excel program as possible. Please search the interference databases as well.

Thanks,
Doug Schultz

James Douglas Schultz, PhD

AU 1635 (Biotechnology)

Patent Examiner

United States Patent and Trademark Office

(Office) REM 2D18

(Mail) REM 2C18

(571) 272-0763

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 133643

TO: James Schultz
Location: REM/2D18/2C18
Art Unit: 1635
Monday, September 27, 2004

Case Serial Number: 09/731457

From: David Schreiber
Location: Biotech-Chem Library
Remsen E01A61
Phone: 272-2526

david.schreiber@uspto.gov

Search Notes

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SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is ____.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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OM nucleic - nucleic search, using sw model

Run on: September 27, 2004, 09:09:27 ; Search time 0.001 Seconds
(without alignments)
2.440 Million cell updates/sec

Title: US-09-731-457B-73
Perfect score: 20
Sequence: 1 cctgtgctgcttctgtctt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 segs, 61 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : rge73.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	15.2	76.0	20	1 AR343622	ACCESSION:AR343622
C 2	13.8	69.0	20	1 AR226061	ACCESSION:AR226061
C 3	13.8	69.0	21	1 AX094846	ACCESSION:AX094846

ALIGNMENTS

RESULT 1
AR343622/c 20 bp DNA linear PAT 17-AUG-2003
LOCUS AR343622
DEFINITION Sequence 12 from patent US 6579850.
ACCESSION AR343622
VERSION AR343622.1 GI:33739398
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nabeshima,Y., Kurao,M., Sekine,S. and Iida,A.
TITLE Polypeptide, novel DNA and novel antibody
JOURNAL Patent: US 6579850-A 12 17-JUN-2003;
FEATURES
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 76.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 0.71;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCTGTGCTGCTTCTGTCTT 20
||||| ||| ||| ||| ||| |||

Db 20 CCTGAGCAGCTTCTGTCTT 1

RESULT 2
AR226061/c 20 bp DNA linear PAT 20-DEC-2002
LOCUS AR226061
DEFINITION Sequence 124 from patent US 6444465.
ACCESSION AR226061
VERSION AR226061.1 GI:27264215
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt,J. and Freier,S.M.
TITLE Antisense modulation of Her-1 expression
JOURNAL Patent: US 6444465-A 124 03-SEP-2002;
FEATURES
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 69.0%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 0.99;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GTGGCTGCTTCTGTCTT 20
Db 20 GTGGCTGCTTATGTCTT 4
||||| ||| ||| ||| |||

RESULT 3
AX094846 21 bp DNA linear PAT 30-MAR-2001
LOCUS AX094846
DEFINITION Sequence 24 from Patent WO0118250.
ACCESSION AX094846
VERSION AX094846.1 GI:13511049
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 24 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 69.0%; Score 13.8; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.95;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCTGTGCTGCTTCTGTCTT 19
Db 3 CCTGTGCTGCTTCTGTCTT 21
||||| ||| ||| ||| ||| |||

Search completed: September 27, 2004, 09:09:27
Job time : 0.001 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 27, 2004, 09:10:38 ; Search time 0.001 Seconds
(without alignments)
3.240 Million cell updates/sec

Title: US-09-731-457B-73
Perfect score: 20
Sequence: 1 cctgtgctgtctgtctt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 81 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4 summaries

Database : rng73.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	Human damage speci
2	15.2	76.0	20	1	Primer 2 for agcin
3	14.2	71.0	21	1	Human gene single
4	13.8	69.0	20	1	Human Her-1 antisense

ALIGNMENTS

RESULT 1
ABS59772
ID ABS59772 standard; DNA; 20 BP.

AC ABS59772;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human damage specific DNA binding protein 1 antisense oligo #64.
XX
KW Antisense; cytosaltic; hepatocarcinoma; antiinflammatory; virucide;
KM Damage-specific DNA-binding protein 1; p127; cancer; human; ss;
KW hyperproliferative disorder; haematopoietic cancer; hepatitis.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= m5c
FT /note= "All cytosines are 5-methyl cytosine"
FT modified_base 1..20
FT /tag= c

FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone"
FT 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl nucleotide"
FT 16..20
FT /tag= d
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl nucleotide"

FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone"
FT 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl nucleotide"
FT 16..20
FT /tag= d
FT /mod_base= OTHER
FT /note= "OTHER= 2'-O-methoxyethyl nucleotide"

WT0200246206-A1.

13-JUN-2002.

04-DEC-2001; 2001WO-US046485.

06-DEC-2000; 2000US-00731457.

(ISIS-) ISIS PHARM INC.

Popoff I, Wyatt JR;

WPI; 2002-599454/64.

Novel antisense compound targeted to nucleic acid molecule encoding
Damage-specific DNA-binding protein 1, p127, useful for treating animal
having disease associated with the protein such as liver cancer, or
hepatitis.

Page 91; Claim 3; 121pp; English.

This invention relates to a novel antisense compound 8 to 50 nucleobases
in length targeted to nucleic acid molecule encoding Damage-specific DNA-
binding protein 1, p127 where the antisense compound specifically
hybridises with and inhibits expression of the damage specific DNA
binding protein-1 gene. The compounds of the invention may be used in
antisense therapy as an inhibitor of expression of damage-specific DNA-
binding protein 1, p127. The antisense compounds of the invention are
useful for inhibiting the expression of damage specific DNA binding
protein 1, p127 in cells or tissues and are also useful for treating an
animal having a disease or condition associated with expression of p127,
such as a hyperproliferative disorder (e.g., cancer such as breast, skin,
liver, or haematopoietic cancer), or hepatitis, by inhibiting the
expression of p127. All antisense oligonucleotides of the invention are
chimeric oligonucleotides (gapmers) 20 nucleotides in length, composed of
a central gap region consisting of ten 2'-deoxynucleotides, which are
flanked on both sides (5' and 3' directions) by five- nucleotide wings.
The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The
internucleoside (backbone) linkages are phosphorothioate (P-S) throughout
the oligonucleotide and all cytidine residues are 5-methylcytidines. The
present sequence represents a damage-specific DNA binding protein 1, p127
antisense oligonucleotide of the invention

Sequence 20 BP; 0 A; 5 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Gaps 0;

Matches 20; Conservative 0; Indels 0; Gaps 0;
Oy 1 CCTGTGCTGTCTGTCTT 20
Db 1 CCTGTGCTGTCTGTCTT 20

RESULT 2

AAV39133/c
ID AAV39133 standard; DNA; 20 BP.

AAV39133;

17-NOV-1998 (first entry)

XX

DE Primer 2 for ageing-retarding activity polypeptide encoding cDNA.
 XX Ageing-retarding activity; ligand; receptor; screening; inhibitor;
 KM augments; premature ageing; Down's syndrome; Turner's syndrome;
 KM Werner's disease; Rosamond-Thomson disease; gene therapy; livestock;
 KM domestic animal; human; mouse; PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 OS Mus sp.
 PN W09829544-A1.
 XX 09-JUL-1998.
 PD 1
 PF 12-DEC-1997; 97WO-JP004585.
 XX 26-DEC-1996; 96JP-00347871.
 PR 31-JUL-1997; 97JP-00205815.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX
 PI Nabeshima Y, Kurao M, Sekine S, Iida A;
 DR WPI; 1998-388125/33.
 XX
 PT Polypeptide which retards ageing - for diagnosis and treatment of ageing-
 PT related diseases and for improvement of livestock breeds.
 XX
 PS Example 4; Page 173; 225pp; Japanese.
 XX
 CC Sequences shown in AAV39132 to V39150 represent PCR primers used in the
 CC course of the invention for amplifying nucleic acid sequences (AAV39127
 CC to AAV39131) encoding polypeptides (AAW63671 to AAW63675) with ageing-
 CC retarding activity. Expression vectors comprising the nucleic acid
 CC sequences can be used to transform host cells for the recombinant
 CC production of such polypeptides. The peptides and their fragments may be
 CC used for investigating possible ligands and receptors which bind to them,
 CC and for screening potential inhibitors of binding of the peptides to
 CC these ligands and receptors. They can also be used for screening
 CC potential augmenters and modifiers of expression of the genes coding for
 CC the peptides. They are used in the treatment and prevention of diseases
 CC involving premature aging, such as Down's syndrome, Turner's syndrome,
 CC Werner's disease, or Rosamond-Thomson disease, and of other diseases of
 CC adults, by administering the peptides or of binding inhibitors or gene
 CC expression modifiers identified by screening as above or by gene therapy.
 CC Gene therapy may also be used for producing improved stock of domestic
 CC animals and livestock
 CC
 SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 XX
 QY
 Db 1 CCTGTGCTGCTGCTT 20
 20 CCTGAGCGAGCTTCTGCTT 1
 Query Match 76.0%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.4;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 RESULT 3
 AAF95259
 ID AAF95259 standard; DNA; 21 BP.
 XX
 AC AAF95259;
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #20.
 XX
 KM Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KM polymorphism; vascular disease; coronary artery disease; forensics;
 KM myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KM

KM pulmonary embolism; paternity test; ds.
 XX
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Variation replace(11,A)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN W0200118250-A2.
 XX 15-MAR-2001.
 PD
 PF 07-SEP-2000; 2000WO-US024503.
 XX
 PR 10-SEP-1999; 99US-0153357P.
 PR 26-JUL-2000; 2000US-0220947P.
 PR 16-AUG-2000; 2000US-0225724P.
 XX
 PA (WHEB) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 DR WPI; 2001-226749/23.
 XX
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.
 XX
 PS Example; Page 48; 242pp; English.
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensic, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification
 CC
 SQ Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
 XX
 QY
 Db 1 CCTGTGCTGCTGCTT 19
 3 CCTTCTGAGTCTGCTT 21
 Query Match 71.0%; Score 14.2; DB 1; Length 21;
 Best Local Similarity 84.2%; Pred. No. 1.6;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 RESULT 4
 AAD36610/c
 ID AAD36610 standard; DNA; 20 BP.
 XX
 AC AAD36610;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Human Her-1 antisense oligonucleotide ISIS #128472.
 XX
 KM Human; epidermal growth factor receptor; hyperproliferative disease;
 KM Her1; antisense; prophylaxis; psoriasis; phosphorothioate backbone;
 KM tumour; cancer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

Search completed: September 27, 2004, 09:10:39
 Job time : 0.001 secs

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FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 8
FT /*tag= d
FT /mod_base= m5c
FT modified_base 13
FT /*tag= e
FT /mod_base= m5c
FT modified_base 14
FT /*tag= f
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"
FT modified_base 17
FT /*tag= g
FT /mod_base= m5c
FT modified_base 18
FT /*tag= h
FT /mod_base= m5c
FT modified_base 20
FT /*tag= i
FT /mod_base= m5c
PN WO200226758-A1.
XX
XX
XX 04-APR-2002.
XX
XX
XX 28-SEP-2001; 2001WO-US030551.
XX
XX
XX 29-SEP-2000; 2000US-00676610.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Wyatt JR, Freier SM;
XX WPI; 2002-394234/42.
XX
XX
XX Novel antisense oligonucleotide that specifically hybridizes with and
XX inhibits nucleic acid encoding epidermal growth factor receptor, useful
XX for treating hyperproliferative disease such as cancer or psoriasis.
XX
XX Claim 1; Page 46; 16pp; English.
XX
XX The invention relates to an antisense oligonucleotide targeted to a
XX nucleic acid molecule encoding human epidermal growth factor receptor
XX (Her1) to inhibit its expression. The antisense compounds are useful for
XX treating diseases or conditions associated with Her-1 such as
XX hyperproliferative diseases especially cancer (lung, ovarian, colon or
XX prostate cancer) and psoriasis. They are also useful as research
XX reagents, diagnostics, therapeutics, kits and prophylactically e.g. to
XX prevent or delay tumour formation. The present sequence is an antisense
XX oligonucleotide targeted to human Her-1
XX
SQ Sequence 20 BP; 8 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.8;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTGCTGCTCTGCTT 20
DB 20 GTGCTGCTTATGCTT 4

```



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OM nucleic - nucleic search, using sw model

Run on: September 27, 2004, 09:11:44 ; Search time 0.001 Seconds
(without alignments)
1.600 Million cell updates/sec

Title: US-09-731-457B-73

Perfect score: 20
Sequence: 1 cctgtgctgtctgtctgtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 segs, 40 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 2 summaries

Database: rn173.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.2	76.0	20	1	US-09-344-510B-12
C 2	13.8	69.0	20	1	US-09-676-610B-124

ALIGNMENTS

RESULT 1
US-09-344-510B-12/C
; Sequence 12, Application US/09344510B
; Patent No. 6579850
; GENERAL INFORMATION:
; APPLICANT: Nabeshima, Youichi
; Kuroo, Makoto
; Sekine, Susumu
; Iida, Akihiro
TITLE OF INVENTION: No. 6579850el Polypeptide, No. 6579850el DNA and No. 6579850
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 1.44 mb, DS, DD
COMPUTER: Compaq Deskpro EN
OPERATING SYSTEM: Windows 98
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344.510B
FILING DATE: 25-Jun-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP97/04585
FILING DATE: 12-DEC-1997
APPLICATION NUMBER: JP 347871
FILING DATE: 26-DEC-1996
APPLICATION NUMBER: JP 205815
FILING DATE: 31-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Perry, Lawrence S.
REGISTRATION NUMBER: 31865
REFERENCE/DOCKET NUMBER: 766.32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 218-2100
TELEFAX: (212) 218-2200
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-344-510B-12

Query Match 76.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CCTGTGCTGTCTGTCTT 20
Db 20 CCTGAGCAGCTTCTGTCTT 1

RESULT 2
US-09-676-610B-124/C
; Sequence 124, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; Applicant: Jacqueline Wyatt
; Applicant: Susan M. Freiler
TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
FILE REFERENCE: RTS-0138
CURRENT APPLICATION NUMBER: US/09/676.610B
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 124
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Antisense Oligonucleotide
US-09-676-610B-124

Query Match 69.0%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GTGCTGTCTGTCTT 20
Db 20 GTGCTGTATGTCTT 4

Search completed: September 27, 2004, 09:11:44
Job time: 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: September 27, 2004, 09:13:31 ; Search time 0.001 Seconds
(without alignments)
4.000 Million cell updates/sec

Title: US-09-731-457B-73
Perfect score: 20
Sequence: 1 cctgtgctgtctgtctt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 5 seqs, 100 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 20
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5 summaries

Database: rnpb73.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-09-731-457B-73
2	15.2	76.0	20	1	US-10-411-253-12
3	14.4	72.0	20	1	US-10-300-263-48
4	14.4	72.0	20	1	US-10-300-263-123
5	13.8	69.0	20	1	US-10-380-931-124

ALIGNMENTS

RESULT 1
US-09-731-457B-73
; Sequence 73, Application US/09731457B
; Patent No. US20020103146A1
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1, P1
; FILE REFERENCE: RTS-0182
; CURRENT APPLICATION NUMBER: US/09/731.457B
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-731-457B-73
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.62;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGTGCTGTCTGTCTT 20
DB 1 CCTGTGCTGTCTGTCTT 20

RESULT 2
US-10-411-253-12/C
; Sequence 12, Application US/10411253
; Publication No. US20030176348A1
; GENERAL INFORMATION:
; APPLICANT: Nabeshima, Youichi
; Kuroo, Makoto
; Sekine, Susumu
; Iida, Akihiro
; TITLE OF INVENTION: No. US20030176348A1 Polypeptide, No. US20030176348A1e1
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 1.44 mb, DS, DD
; COMPUTER: Compaq Deskpro EM
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Wordpad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/411.253
; FILING DATE: 11-Apr-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/344.510B
; FILING DATE: 25-Jun-1999
; APPLICATION NUMBER: PCT/JP97/04585
; FILING DATE: 12-DEC-1997
; APPLICATION NUMBER: JP 347871
; FILING DATE: 26-DEC-1996
; APPLICATION NUMBER: JP 205815
; FILING DATE: 31-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-411-253-12
Query Match 76.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.6;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCTGTGCTGTCTGTCTT 20
DB 20 CCTGAGCAGCTTCTGTCTT 1
RESULT 3
US-10-300-263-48
; Sequence 48, Application US/10300263
; Publication No. US20040096834A1
; GENERAL INFORMATION:

